



## SEQUENCE LISTING

<110> CROCE, Carlo M.  
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<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN  
FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

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Lys	Leu	Asn	Arg	Tyr	Ser	Asp	Gly	Leu	Leu	Arg	Phe	Gly	Phe	Ser	Gln
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<212> DNA

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cgctgcaggg	acgagctgga	gggcccggag	cccaaaggcg	gcaacaagct	caagcaggcc	960
tcgcagaaga	gccagcgcgc	gcagcaggtc	ctgcacctgc	aggtactgca	gcttcagcag	1020
gagaagcggc	agctccggca	ggagctcgag	agcctcatga	aggagcagga	cctgctggag	1080
accaagctca	ggtcctacga	gagggagaag	accagcttcg	gccccgcgct	ggaggagacc	1140
cagtgggagg	tgtgccagaa	gtcaggcgag	atctccctcc	tgaagcagca	gctgaaggag	1200
tcccagacgg	aggtgaacgc	caaggctagc	gagatcctgg	gtctcaaggc	acagctgaag	1260
gacacgcggg	gcaagctgga	gggcctggag	ctgaggaccc	aggacctgga	gggcgcctcg	1320
cgcaccaagg	gcctggagct	ggaggtctgt	gagaatgagc	tgcagcagag	ctacgtggcc	1380
atgtaccagc	ggaaccagcg	cctggagaag	gccctgcagc	agctggcacg	tggggacagc	1440
gccggggagc	ccttggagggt	tgacctggaa	ggggctgaca	tcccctacga	ggacatcata	1500
gccactgaga	tc					1512

<210> 13  
<211> 1692  
<212> DNA  
<213> Homo sapiens

<400> 13  
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tcgcagtaca agctgcgcaa gtctctccac ctcaagaagc tcaaccggta ttccgacggg 120  
ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180  
aagagcgaag acttcttcta catcaaggtc agccagaaag cccggggctc ccatcaccca 240  
gattacacgg cactgtccag cggggattta gggggccagg ctggggtgga ctttgacccg 300  
tccacacccc ccaagctcat gcccttctcc aatcagctag aaatgggctc cgagaagggt 360  
gcagtgaggc ccacagcctt caagcctgtg ctgccacggc caggagccat cctgcactcc 420  
tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480  
gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540  
agcctgcccc cacacagcac cagcagcagc taccagctgg acccgctggg cacacccgtg 600  
ggaccacaaa gccgttttgg gggctccgcc cacaacatca cccagggcat cgtcctccag 660  
gacagcaaca tgatgagcct gaaggctctg tccttctccg acggaggtag caagctgggc 720  
cactcgaaca aggcagacaa gggcccctcg tgtgtccgct ccccatctc cacggacgag 780  
tgcagcatcc aggagctgga gcagaagctg ttggagaggg agggcgccct ccagaagctg 840  
cagcgcagct ttgaggagaa ggagcttgcc tccagcctgg cctacgagga gcggccgcgg 900  
cgctgcaggg acgagctgga gggcccggag cccaaaggcg gcaacaagct caagcaggcc 960  
tcgcagaaga gccagcgcgc gcagcaggtc ctgcacctgc aggtactgca gcttcagcag 1020  
gagaagcggc agctccggca ggagctcgag agcctcatga aggagcagga cctgctggag 1080  
accaagctca ggtcctacga gagggagaag accagcttcg gccccgcgct ggaggagacc 1140  
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tcccagacgg aggtgaacgc caaggctagc gagatcctgg gtctcaaggc acagctgaag 1260  
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cgcaccaagg gcttgagct ggaggtctgt gagaatgagc tgcagcga gaagaacgag 1380  
gcggagctgc tgcgggagaa ggtgaacctg ctggagcggc tgcgggcca gctgcgggag 1440  
gagcggcaag gccatgacca gatgtcctcg ggcttccagc atgagcggct cgtgtggaag 1500  
gaggagaagg agaaggtgat tcagtaccag aaacagctgc agcagagcta cgtggccatg 1560  
taccagcgga accagcgcct ggagaaggcc ctgcagcagc tggcacgtgg ggacagcgcc 1620  
ggggagccct tggaggttga cctggaaggg gctgacatcc cctacgagga catcatagcc 1680  
actgagatct ga 1692

<210> 14  
<211> 1722  
<212> DNA  
<213> Homo sapiens

<400> 14  
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ctgctgaggt ttggcttctc ccaggactcc ggtcacggca agtccagctc caaaatgggc 180  
aagagcgaag acttcttcta catcaaggtc agccagaaag cccggggctc ccatcaccca 240  
gattacacgg cactgtccag cggggattta gggggccagg ctggggtgga ctttgacccg 300  
tccacacccc ccaagctcat gcccttctcc aatcagctag aaatgggctc cgagaagggt 360  
gcagtgaggc ccacagcctt caagcctgtg ctgccacggc caggagccat cctgcactcc 420  
tccccggaga gtgccagcca ccagctgcac cccgcccctc cagacaagcc caaggagcag 480  
gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540  
agcctgcccc cacacagcac cagcagcagc taccagctgg acccgctggg cacacccgtg 600  
ggaccacaaa gccgttttgg gggctccgcc cacaacatca cccagggcat cgtcctccag 660  
gacagcaaca tgatgagcct gaaggctctg tccttctccg acggaggtag caagctgggc 720

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cactcgaaca aggcagacaa gggccctcg tgtgtccgct ccccatctc cacggacgag 780
tgcagcatcc aggagctgga gcagaagctg ttggagaggg agggcgccct ccagaagctg 840
cagcgcagct ttgaggagaa ggagcttgcc tccagcctgg cctacgagga gcggccgcgg 900
cgctgcaggg acgagctgga gggcccgag cccaaaggcg gcaacaagct caagcaggcc 960
tcgcagaaga gccagcgcgc gcagcaggtc ctgcacctgc aggtactgca gcttcagcag 1020
gagaagcggc agctccggca ggagctcgag agcctcatga aggagcagga cctgctggag 1080
accaagctca ggtcctacga gagggagaag accagcttcg gccccgcgct ggaggagacc 1140
cagtgggagg tgtgccagaa gtcaggcgag atctccctcc tgaagcagca gctgaaggag 1200
tcccagacgg aggtgaacgc caaggctagc gagatcctgg gtctcaaggc acagctgaag 1260
gacacgctgg gcaagctgga gggcctggag ctgaggaccc aggacctgga gggcgccctg 1320
cgcaccaagg gcctggagct ggaggtctgt gagaatgagc tgcagcgcaa gaagaacgag 1380
gcggagctgc tgcgggagaa ggtgaacctg ctggagcagg agctgcagga gctgcgggcc 1440
caggccgccc tggcccgcga catggggccg cccaccttcc ccgaggacgt ccctgccctg 1500
cagcgggagc tggagcggct cgtgtggaag gaggagaagg agaaggatgat tcagtaccag 1560
aaacagctgc agcagagcta cgtggccatg taccagcgga accagcgct ggagaaggcc 1620
ctgcagcagc tggcacgtgg ggacagcgcc ggggagccct tggaggttga cctggaaggg 1680
gctgacatcc cctacgagga catcatagcc actgagatct ga 1722

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<210> 15  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

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<400> 15
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1             5             10             15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20             25             30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
             35             40             45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser
  50             55             60

Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg Arg
  65             70             75

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<210> 16  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

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<400> 16
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys
  1             5             10             15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys
             20             25             30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln
             35             40             45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp

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50					55					60					
Phe	Phe	Tyr	Ile	Lys	Val	Ser	Gln	Lys	Ala	Arg	Gly	Ser	His	His	Pro
65					70					75					80
Asp	Tyr	Thr	Ala	Leu	Ser	Ser	Gly	Asp	Leu	Gly	Gly	Gln	Ala	Gly	Val
				85					90					95	
Asp	Phe	Asp	Pro	Ser	Thr	Pro	Pro	Lys	Leu	Met	Pro	Phe	Ser	Asn	Gln
			100					105					110		
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys
		115					120					125			
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser
		130				135					140				
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln
145					150					155					160
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg
				165					170					175	
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Ala	Gly	Glu	Pro	Leu	Glu
			180					185					190		
Val	Asp	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Tyr	Glu	Asp	Ile	Ile	Ala	Thr
		195					200					205			
Glu	Ile														
	210														

<210> 17  
 <211> 537  
 <212> PRT  
 <213> Homo sapiens

<400> 17															
Met	Gly	Ser	Val	Ser	Ser	Leu	Ile	Ser	Gly	His	Ser	Phe	His	Ser	Lys
1				5					10					15	
His	Cys	Arg	Ala	Ser	Gln	Tyr	Lys	Leu	Arg	Lys	Ser	Ser	His	Leu	Lys
			20					25					30		
Lys	Leu	Asn	Arg	Tyr	Ser	Asp	Gly	Leu	Leu	Arg	Phe	Gly	Phe	Ser	Gln
		35					40					45			
Asp	Ser	Gly	His	Gly	Lys	Ser	Ser	Ser	Lys	Met	Gly	Lys	Ser	Glu	Asp
		50				55					60				
Phe	Phe	Tyr	Ile	Lys	Val	Ser	Gln	Lys	Ala	Arg	Gly	Ser	His	His	Pro
65					70					75					80
Asp	Tyr	Thr	Ala	Leu	Ser	Ser	Gly	Asp	Leu	Gly	Gly	Gln	Ala	Gly	Val
				85					90					95	

Asp	Phe	Asp	Pro	Ser	Thr	Pro	Pro	Lys	Leu	Met	Pro	Phe	Ser	Asn	Gln		
			100					105					110				
Leu	Glu	Met	Gly	Ser	Glu	Lys	Gly	Ala	Val	Arg	Pro	Thr	Ala	Phe	Lys		
		115					120					125					
Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser		
	130					135					140						
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln		
145					150					155					160		
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg		
				165					170					175			
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln		
			180					185						190			
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly		
	195						200					205					
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met		
	210					215					220						
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly		
225					230					235					240		
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile		
			245					250						255			
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu		
		260					265						270				
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu		
	275						280					285					
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp		
	290					295					300						
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala		
305					310					315					320		
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu		
				325					330					335			
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu		
			340					345					350				
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg		
		355					360					365					
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val		
	370					375					380						
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu		
385					390					395					400		

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
 405 410 415  
 Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
 420 425 430  
 Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
 435 440 445  
 Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
 450 455 460  
 Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val  
 465 470 475 480  
 Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln  
 485 490 495  
 Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp  
 500 505 510  
 Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro  
 515 520 525  
 Tyr Glu Asp Ile Ile Ala Thr Glu Ile  
 530 535

<210> 18  
 <211> 504  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
 1 5 10 15  
 His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
 20 25 30  
 Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
 35 40 45  
 Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
 50 55 60  
 Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
 65 70 75 80  
 Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
 85 90 95  
 Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
 100 105 110  
 Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
 115 120 125



Pro	Val	Leu	Pro	Arg	Ser	Gly	Ala	Ile	Leu	His	Ser	Ser	Pro	Glu	Ser	130	135	140
Ala	Ser	His	Gln	Leu	His	Pro	Ala	Pro	Pro	Asp	Lys	Pro	Lys	Glu	Gln	145	150	155
Glu	Leu	Lys	Pro	Gly	Leu	Cys	Ser	Gly	Ala	Leu	Ser	Asp	Ser	Gly	Arg	165	170	175
Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	180	185	190
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	195	200	205
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	210	215	220
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	225	230	235
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	245	250	255
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	260	265	270
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	275	280	285
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	290	295	300
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	305	310	315
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	325	330	335
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	340	345	350
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	355	360	365
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	370	375	380
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	385	390	395
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys	405	410	415
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg	420	425	430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg  
450 455 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser  
465 470 475 480

Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr  
485 490 495

Glu Asp Ile Ile Ala Thr Glu Ile  
500

<210> 19

<211> 563

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Ser Tyr Gln

180					185					190					
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly
	195						200					205			
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met
	210					215					220				
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly
225					230					235					240
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile
				245					250					255	
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu
			260					265						270	
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu
		275					280					285			
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp
	290					295					300				
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala
305					310					315					320
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu
				325					330					335	
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu
			340					345					350		
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg
		355					360					365			
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val
	370					375					380				
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu
385					390					395					400
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys
				405					410					415	
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg
			420					425					430		
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu
		435					440					445			
Val	Cys	Glu	Asn	Glu	Leu	Gln	Arg	Lys	Lys	Asn	Glu	Ala	Glu	Leu	Leu
	450					455					460				
Arg	Glu	Lys	Val	Asn	Leu	Leu	Glu	Arg	Leu	Arg	Ala	Glu	Leu	Arg	Glu
465					470					475					480
Glu	Arg	Gln	Gly	His	Asp	Gln	Met	Ser	Ser	Gly	Phe	Gln	His	Glu	Arg

485

490

495

Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln  
500 505 510

Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu  
515 520 525

Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu  
530 535 540

Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala  
545 550 555 560

Thr Glu Ile

<210> 20

<211> 573

<212> PRT

<213> Homo sapiens

<400> 20

Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
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His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn	Ser	Met	Ser	Ser	Leu	Pro	Thr	His	Ser	Thr	Ser	Ser	Ser	Tyr	Gln	180	185	190	
Leu	Asp	Pro	Leu	Val	Thr	Pro	Val	Gly	Pro	Thr	Ser	Arg	Phe	Gly	Gly	195	200	205	
Ser	Ala	His	Asn	Ile	Thr	Gln	Gly	Ile	Val	Leu	Gln	Asp	Ser	Asn	Met	210	215	220	
Met	Ser	Leu	Lys	Ala	Leu	Ser	Phe	Ser	Asp	Gly	Gly	Ser	Lys	Leu	Gly	225	230	235	240
His	Ser	Asn	Lys	Ala	Asp	Lys	Gly	Pro	Ser	Cys	Val	Arg	Ser	Pro	Ile	245	250	255	
Ser	Thr	Asp	Glu	Cys	Ser	Ile	Gln	Glu	Leu	Glu	Gln	Lys	Leu	Leu	Glu	260	265	270	
Arg	Glu	Gly	Ala	Leu	Gln	Lys	Leu	Gln	Arg	Ser	Phe	Glu	Glu	Lys	Glu	275	280	285	
Leu	Ala	Ser	Ser	Leu	Ala	Tyr	Glu	Glu	Arg	Pro	Arg	Arg	Cys	Arg	Asp	290	295	300	
Glu	Leu	Glu	Gly	Pro	Glu	Pro	Lys	Gly	Gly	Asn	Lys	Leu	Lys	Gln	Ala	305	310	315	320
Ser	Gln	Lys	Ser	Gln	Arg	Ala	Gln	Gln	Val	Leu	His	Leu	Gln	Val	Leu	325	330	335	
Gln	Leu	Gln	Gln	Glu	Lys	Arg	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	340	345	350	
Met	Lys	Glu	Gln	Asp	Leu	Leu	Glu	Thr	Lys	Leu	Arg	Ser	Tyr	Glu	Arg	355	360	365	
Glu	Lys	Thr	Ser	Phe	Gly	Pro	Ala	Leu	Glu	Glu	Thr	Gln	Trp	Glu	Val	370	375	380	
Cys	Gln	Lys	Ser	Gly	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Gln	Leu	Lys	Glu	385	390	395	400
Ser	Gln	Thr	Glu	Val	Asn	Ala	Lys	Ala	Ser	Glu	Ile	Leu	Gly	Leu	Lys	405	410	415	
Ala	Gln	Leu	Lys	Asp	Thr	Arg	Gly	Lys	Leu	Glu	Gly	Leu	Glu	Leu	Arg	420	425	430	
Thr	Gln	Asp	Leu	Glu	Gly	Ala	Leu	Arg	Thr	Lys	Gly	Leu	Glu	Leu	Glu	435	440	445	
Val	Cys	Glu	Asn	Glu	Leu	Gln	Arg	Lys	Lys	Asn	Glu	Ala	Glu	Leu	Leu	450	455	460	
Arg	Glu	Lys	Val	Asn	Leu	Leu	Glu	Gln	Glu	Leu	Gln	Glu	Leu	Arg	Ala	465	470	475	480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp  
485 490 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu  
500 505 510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val  
515 520 525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu  
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Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly  
545 550 555 560

Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile  
565 570

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<211> 591  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: F37 Probe

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tatgggggca tctcttcccc agagaggcac tcagttagcc tcctgtgcct ggccccagtc 180  
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<212> DNA  
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<223> Description of Artificial Sequence: FEZ1 alterable  
region amplificatin primer G12

<400> 22  
gctgccacag cctttccaag acc

23

<210> 23  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G13

<400> 23

taccggttga gcttcttgag gtg

23

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G14.2

<400> 24

acagcttcca cagcaagcac tgc

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<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G15

<400> 25

attggagaag ggcatgagct t

21

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G16

<400> 26

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22

<210> 27

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntABR

<400> 27  
gtttccaacc cacttaccct tgc 23

<210> 28  
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<212> DNA  
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region amplification primer IntABF

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<210> 29  
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<212> DNA  
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region amplification primer G17

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ggcttcagct cctgctcctt gg 22

<210> 30  
<211> 23  
<212> DNA  
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region amplification primer G20

<400> 30  
acaacatcac ccagggcatc gtc 23

<210> 31  
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<212> DNA  
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<220>  
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region amplification primer G21

<400> 31  
cctccagctc gtcctgcag c 21

<210> 32



<211> 23  
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 <213> Artificial Sequence  
  
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 <400> 32  
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 <210> 33  
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 <210> 35  
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 <400> 35  
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 <210> 36  
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<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G1

<400> 36

tgaacgccaa ggctagcgag atc

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<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G2

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gctcctgcag ctctgctcc ag

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<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G75

<400> 38

cccaccttcc ccgaggacgt c

21

<210> 39

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G82

<400> 39

agccccgagga catctgggtca tgg

23

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G5

<400> 40

cctgccctgc agcgggagct ggag

24

<210> 41  
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<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G6

<400> 41  
agctgctgca ggccttctc cag 23

<210> 42  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G7

<400> 42  
cagtaccaga aacagctgca gcagagc 27

<210> 43  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G8

<400> 43  
ccctgcctcc cagtgccagg tc 22

<210> 44  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: First strand  
of partially-double stranded adapter-linker

<400> 44  
gatctcgacg aattcgtgag acct 24

<210> 45  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Second strand  
of partially-double stranded adapter-linker

<400> 45

tggtctcacg aattcgtcga

20

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

<400> 46

tcccaggact ccggtcacgg caa

23

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 47

gagcggcaag gccatgacca g

21

<210> 48

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

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agcctgcca cacacagcac cag

23

<210> 49

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 49  
cagcgccggg gagcccttgg a 21

<210> 50  
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<220>  
<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

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gtgagaatga gctgcagcgc aag 23

<210> 51  
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<212> DNA  
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<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 51  
cagcagagct acgtggccat gt 22

<210> 52  
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<212> DNA  
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<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

<400> 52  
agctgctgcg ggagaagggtg aac 23

<210> 53  
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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 53  
cagcatgagc ggctcgtgtg ga 22

<210> 54  
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 <223> Description of Artificial Sequence: Donor site  
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 <400> 54  
 aggtgaacct gctggagcag gag 23  
  
 <210> 55  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Acceptor site  
           sequence of truncated FEZ1 truncation region  
  
 <400> 55  
 gagcggctgc gggccgagct gc 22  
  
 <210> 56  
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 <212> DNA  
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 <223> Description of Artificial Sequence: Donor site  
           sequence of truncated FEZ1 truncation region  
  
 <400> 56  
 ctgcagcggg agctggagcg gctg 24  
  
 <210> 57  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Acceptor site  
           sequence of truncated FEZ1 truncation region  
  
 <400> 57  
 gagcggctcg tgtggaagga g 21  
  
 <210> 58  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for  
amplifying FEZ1 cDNA

<400> 58

cagatgggca gcgtcagtag cctcatc

27

<210> 59

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for  
amplifying FEZ1 cDNA

<400> 59

tcagatctca gtggctatga tgtc

24

<210> 60

<211> 8073

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide  
sequence of vector pQBI-AdCMV5-IRES-GFP

<400> 60

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gtggcggaag	tgtgatgttg	caagtgtggc	ggaacacatg	taagcgacgg	atgtggcaaa	180
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